

GenCore version 5.1.3
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match Length	DB ID	Description			
1	14.04	100.0	3026	3	AF324424	Ichthyoph	
2	254.4	18.1	1520	3	AF405431	Ichthyoph	
3	252.6	18.0	2486	3	AF140273	Ichthyoph	
4	214.6	15.3	1249	3	M92907	Ichthyoph	
5	96	6.8	175748	2	AC120669	Rattus no	
6	96	6.8	180903	2	AC125859	Rattus no	
7	95.2	6.8	186232	2	AC02322	Homo sapi	
8	92.4	6.6	179553	2	AC024253	Homo sapi	
9	90.8	6.5	131274	2	AC096869	Rattus no	
10	90.8	6.5	176822	2	AC091174	Rattus no	
11	85.6	6.1	261604	2	AC119819	Mus muscu	
12	85.4	6.1	127194	2	AC117014	Rattus no	
13	85.4	6.1	155019	2	AC117361	Rattus no	
14	81	5.8	35793	5	AY016024	Takifugu	
15	81	5.8	84472	2	AC096684	Takifugu	
16	80.2	5.7	132449	9	AL365212	Human DNA	
17	77.2	5.5	23238	5	AJ271723	Fugu rubr	
18	77	5.5	85786	9	AL162582	Human DNA	
19	76.6	5.5	10115	5	AF397467	Ichthurus	
20	75.8	5.4	183113	2	AC131200	Rattus no	
21	75.6	5.4	170932	2	AC096032	Rattus no	
22	74.6	5.3	204259	2	AC10817	Mus muscu	
23	74	5.3	172037	2	AC044842	Homo sapi	
24	72.4	5.2	189627	2	AC119627	Rattus no	
25	72.4	5.2	191841	2	AC121274	Rattus no	
26	72	5.1	134558	2	AC125757	Rattus no	
27	72	5.1	180568	2	AC020857		
28	69.8	5.0	172039	2	AF01305052		
29	69.2	4.9	172553	2	AC084361		
30	68.2	4.9	71553	2	AC096997		
31	68	4.8	154141	2	AC121042	Rattus no	
32	68	4.8	162659	9	AC00097	Homo sapi	
33	67.8	4.8	184330	2	AC113220	Rattus no	
34	67.2	4.8	185994	2	AC002042	Homo sapi	
35	67.2	4.8	300594	2	AC129317	Mus muscu	
36	66.2	4.7	131346	2	AC119558	Rattus no	
37	66	4.7	158415	2	AC117835	Rattus no	
38	65.8	4.7	101534	2	AC108576	Rattus no	
39	65.8	4.7	298383	3	AE033782	Drosophil	
40	64.8	4.6	177635	2	AC094443		
41	64.4	4.6	186558	2	AC079021		
42	64.4	4.6	325608	2	AC12787	Mus muscu	
43	64.2	4.6	121787	2	AC118993	Rattus no	
44	64	4.6	107617	2	AC116961	Dictyoste	
45	63.8	4.5	177435	2	AC128321	Rattus no	
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Db	1613	ATACATGTTACTGAACTGTTACTAAAGAAATTAACTCTGGGCCACAGCTAAAGTATATGCTG	1674
Qy	1328	CTGCTAAAGAAATATATAATG-----TGATTTGGCTTAATTATTCATTCCT	1378
Db	1673	AAGCTTACTCAGGATAATGGCCCTGCACACTTGGCTATATTTCATTCCT	1732
Qy	1379	TATTTGATTCTCTATTATTATT	1403
Db	1733	TATTTTATTCTCTATTATT	1757
RESULT 4			
LOCUS	ICYMANT	1249 bp	mRNA
DEFINITION	Ichthyophthirius multifiliis immobilization antigen precursor,	linear	INV 18-SEP-1
ORGANISM	mRNA, partial cds.		
ACCESSION	M92907		
VERSION	M92907.1		
KEYWORD	GI:3628568		
SOURCE	Ichthyophthirius multifiliis.		
ORGANISM	Ichthyophthirius multifiliis.		
REFERENCE	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;		
AUTHORS	Hymenostomatida; Ophyryginina; Ichthyophthirius.		
TITLE	1 (bases 1 to 1249)		
JOURNAL	Lin, T. L. and Dickerson, H. W.		
MEDLINE	Purification and partial characterization of immobilization		
PUBLMED	antigens from Ichthyophthirius multifiliis		
PUBLMED	J. Protozool. 39 (4), 457-463 (1992)		
PUBLMED	93020590		
PUBLMED	1383510		
REFERENCE	2 (bases 1 to 1249)		
AUTHORS	Clark, T. G., McGraw, R. A. and Dickerson, H. W.		
TITLE	Developmental expression of surface antigen genes in the parasite		
JOURNAL	Direct Ichthyophthirius multifiliis		
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 89 (14), 6363-6367 (1992)		
PUBLMED	92338298		
REFERENCE	3 (bases 1 to 1249)		
AUTHORS	Clark, T.		
TITLE	Direct Submission		
JOURNAL	Submitted (06-JUN-1992) Microbiology and Immunology, Cornell		
MEDLINE	University, Ithaca, NY 14853, USA		
PUBLMED	1631132		
REFERENCE	4 (bases 1 to 1249)		
AUTHORS	Clark, T.		
TITLE	Direct Submission		
JOURNAL	Submitted (18-SEP-1998) Microbiology and Immunology, Cornell		
MEDLINE	University, Ithaca, NY 14853, USA		
REFERENCE	Sequence update by submitter		
AUTHORS	Clark, T.		
TITLE	On Sep 18, 1998 this sequence version replaced gi:159289.		
JOURNAL	Location/Qualifiers		
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	177..893		
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/rp_unit=414..680			
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Best Local Similarity	55.4%	Pred. No. 3.2e 28;	
Matches	591;	Conservative 0;	Missmatches 374;
		Indels 102;	Gaps 5;
Qy	344 GTGTAAATTCTAGAATTAAATTCTATAATGAAATGCTICAATTTATGCCAGGTGCTA	403	
Db	112 GTGCTGCTTAAGGAAAGGTAATGTAATTAAACCTTTCGAGCAAAATTAGCTGCTA	171	
Qy	404 GTACATGCACAGCCTGTCGGTAACACAGATTGGTGCATGACTGCTGTAATGCCG	463	
Db	172 GTATATGTTACCATGCCAAATAAACAGTAAAGCTCCTGTTACCAATGAGGTGACT	231	
Qy	464 CTACCATAGTCGATAAATTAAGTCGATGCTTACTGTACTGACTGTGATGGAG	523	
Db	232 CTACTTAAAGCCACATAAAGCAGTACTTAAATGCTCTACTGGCTACTGGACTG	291	
Qy	524 TAACTACTGATTATGTTAGATCATTCAAGAATGTTAAATGTAAGCTTAACTTTACT	583	
Db	292 TGAAGATCTTTGATGATCATTCAAGCCTGTTAAAGTGTAAATGTAAGCTTAAC	351	
Qy	584 ATATGGTAATAATGGTAATACTCCCTTCAATCCAGSTAAGTTAAATGCCACACCTTGT	643	
Db	352 ATATGGCTGTTCTCCTAAGGTGAAGGTCCTGGCTTAAAGTTTGCTGGTGCCTG	411	
Qy	644 CGSCAAATTAAACCTGCT-----		ATG 664
Db	412 CCCCTGAGGTGCTGCCGTTACTAGTTAATGTGTACCTTGCCCAAACTAACAAACAG		471
Qy	665 TTGCTTAAGCTACTTTAGGTAATGATCTACATAACCGCATATACTGAACTGTGCATG		724
Db	472 ATTCCTCTGGCACTGAGGTGCTAACTTATGSCACATAATTTAGCAATTAAATGTC		531
Qy	725 CTGATGGTACTATAAGTCGTCGGAGT--ATAATAATGGTAGGCAAAACACTGTA		781
Db	532 CTACTGGCACTGACTTGTAGTGGGAGTGACACTGTGTTTAATACATGCCACATTA		591
Qy	782 GRACTAATTGTGCTCTAACTTTACATAATAATGCTCTAATT-----		
Db	592 GCTTAAATGCAAGACCTAACTTTACTATAATGGTGTCTCTPAGGGGAAGCTCTG		651
Qy	827 -----		
Db	652 GCGTTAAAGTTTGTGCTGCTGCCGCTGAGCTGCTGCTGACTGCTAATTGATCAT		847
Qy	848 GCCTACCTTGGCCAGCAAATAAGATTATGGTGTGAGCTGCGGCTA 907		
Db	712 GTGTAATTGCTGCCAAATAACCAAAGGATTCCTCTCTCTCTCTCTCTCTCTCT		768
Qy	908 CTTTAGCCAATAATGTAATAATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG		
Db	769 ATTAGGCACATAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG		967
Qy	968 CTAATTGTAATAATGTAATAACAGATGCTTAATTGTGCTGCTGCTGCTGCTGCTG		
Db	829 CACTTGTGTTTGTAGTAATTCTCCACATAATGCTGCTGCTGCTGCTGCTGCTG		1027
Qy	1028 GTAAATAATTCTAGGAGGAAGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG		
Db	889 ATGGTAAATCTCGAAGGAAAGTTAAAGTCTCCAGTAAAGTCTCCAGTAAAC		1087
Qy	1088 GCGCTGAGCAACTGCGGTTACTGCTTAAATGCTAAATGCTGCTGCTGCTGCTG		945

Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S.,
 Osman, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
 Wang, S., Ward-Moore, S., Warren, R., Watlington, C., Watlington, S.,
 Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K.,
 Wu, C., Wu, Y., Wu, Y.-F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstock, G. and Gibbs, R.
 Direct Submission
 Unpublished
 2 (bases 1 to 176822)
 Worley, K. C.
 Direct Submission
 Submitted (09-NOV-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 176822)
 Worley, K. C.
 Direct Submission
 Submitted (12-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 11, 2002 this sequence version replaced gi:18846108.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: G2VY
 Center clone name: CH230-98T1
 ----- Summary Statistics
 Sequencing vector: Plasmid;
 Chemistry: Dye-Terminator Big Dye: 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 115453 bases at least Q40
 Consensus quality: 125051 bases at least Q30
 Consensus quality: 133023 bases at least Q20

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: this is a 'working draft' sequence. It currently
 * consists of 77 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 1052: contig of 1052 bp in length
 * 1053 1152: gap of unknown length
 * 1153 2179: contig of 1027 bp in length
 * 2180 2279: gap of unknown length
 * 2280 3355: contig of 1076 bp in length
 * 3356 3455: gap of unknown length
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 * 4835 4934: gap of unknown length
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 * 6323 7400: contig of 1078 bp in length
 * 7401 7500: gap of unknown length
 * 7501 8807: contig of 1307 bp in length
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 * 8908 10266: contig of 1359 bp in length
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 * 78861 78862: gap of unknown length
 * 78862 81654: contig of 2693 bp in length

Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L17592
 Center clone name: 107_G_22
 ----- Summary statistics
 Sequencing vector: Plasmid; n/a: 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 243729 bases at least Q40
 Consensus quality: 251231 bases at least Q30
 Consensus quality: 253857 bases at least Q20
 Insert size: 220000; agarose-fp
 Insert size: 255004; sum-of-contigs
 Quality coverage: 7.1 in Q20 bases; sum-of-cont
 Quality coverage: 8.2 in Q20 bases; agarose-fp
 Quality coverage: 7.1 in Q20 bases; sum-of-cont

 NOTE: This is a 'working draft' sequence. It currently consists of 67 contigs. Gaps between the contigs are represented as runs of N. The order of the pairs is believed to be correct as given, however the order of the gaps between them are based on estimates provided by the submitter.
 This sequence will be replaced by the finished sequence as soon as it is available.
 the accession number will be preserved.
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 * 642: 741: gap of 100 bp
 * 742: 1156: contig of 415 bp in length
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 * 1257: 1891: contig of 635 bp in length
 * 1892: 1991: gap of 100 bp
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Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	REFERENCE	1	1 (bases 1 to 127354)	
	AUTHORS	Mouny, D.M., Adams, C., Adlo-Oduoia, B., Ali-Osman, F.R., Allen, C., Alisbrooks, S.L., Amaral-Tunng, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Blain, K., Blankenburg, K., Bonin, D., Bouck, J., Bowie, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P., Buhey, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathone, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, J., Deaderick, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Doubtwhite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Edwards, C.C., Elhai, C., Escote, M., Fallas, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, J., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlik, P., Hawes, A., Hernandez, F., Hernandez, O., Hodgson, A., Hogue, M., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Kelly, S., Khan, U., King, L., Korvaj, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, J.C., Lewin, J., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louisege, J., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Madeshwaran, M., Mapua, R., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhinney, B., Mcleod, M.P., Meador, M., Mel, G., Metzker, M., Miner, T., Mitchell, T., Mohabbat, R., Morgan, M., Morris, M., Moser, M., Neal, D., Newson, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokonwo, S., Oguh, M., Okuongu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, B., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshani, N., Sisson, I., Sodergren, E., Sonaike, T., Spars, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, K., Tang, Tansey, J., Taylor, C., Telford, T., Thomas, N., Thomas, N., Thomas, N., Usmani, K., Vasquez, L., Vera, V., Villalon, D.D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington C., Watlington, S., Williams, G., Williamson, A., Wleczky, R., Woeden, S., Wu, Y., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Weinstock, G., and Gibbs, R., Worley, K.C.	TITLE	Submitted (18 JUL 2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, On 3 (bases 1 to 127354)
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	AUTHORS	Worley, K.C.	Direct Submission	
	JOURNAL	Unpublished	Unpublished	
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JOURNAL				
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COMMENT				
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COMMENT				
REFERENCE	12	12 (bases 1 to 127354)		
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REFERENCE	13	13 (bases 1 to 127354)		
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REFERENCE	14	14 (bases 1 to 127354)		
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REFERENCE	15	15 (bases 1 to 127354)		
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REFERENCE	16	16 (bases 1 to 127354)		
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REFERENCE	75	75 (bases 1 to 127354)		
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REFERENCE	76	76 (bases 1 to 127354)		
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REFERENCE	77	77 (bases 1 to 127354)		
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REFERENCE	78	78 (bases 1 to 127354)		
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REFERENCE	79	79 (bases 1 to 127354)		
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REFERENCE	80	80 (bases 1 to 127354)		
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REFERENCE	94	94 (bases 1 to 127354)		
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REFERENCE	95	95 (bases 1 to 127354)		
AUTHORS				
JOURNAL				
COMMENT				
REFERENCE	96	96 (APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, On Jul 14, 2002, this sequence version replaced g1:20066062.		
AUTHORS				
JOURNAL				
COMMENT				
REFERENCE	97	97 (APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, On Jul 14, 2002, this sequence version replaced g1:20066062.		
AUTHORS				
JOURNAL				
COMMENT				
REFERENCE	98	98 (APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, On Jul 14, 2002, this sequence version replaced g1:20066062.		
AUTHORS				
JOURNAL				
COMMENT				
REFERENCE	99	99 (APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, On Jul 14, 2002, this sequence version replaced g1:20066062.		
AUTHORS				
JOURNAL				
COMMENT				
REFERENCE	100	100 (APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, On Jul 14, 2002, this sequence version replaced g1:20066062.		
AUTHORS				
JOURNAL				
COMMENT				
REFERENCE	101	101 (APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, On Jul 14, 2002, this sequence version replaced g1:20066062.		
AUTHORS				

** NOTE: Estimated insert size may differ from sequence length
 ** (see http://www.hgsc.bcm.edu/docs/Genbank_draft_data.html)
 ** NOTE: This is a 'working draft' sequence. It currently
 ** consists of 57 contigs. The true order of the pieces
 ** is not known and their order in this sequence record is
 ** arbitrary. Gaps between the contigs are represented as
 ** runs of N. But the exact sizes of the gaps are unknown.
 ** this record will be updated with the finished sequence
 ** as soon as it is available and the accession number will
 ** be preserved.

1	1478: contig of 1478 bp in length
**	1479: gap of unknown length
**	1579: contig of 1339 bp in length
**	2918: gap of unknown length
**	3018: contig of 1079 bp in length
**	4097: gap of unknown length
**	4198: contig of 1446 bp in length
**	5643: gap of unknown length
**	5743: contig of 1197 bp in length
**	6940: gap of unknown length
**	7040: contig of 1442 bp in length
**	8482: gap of unknown length
**	8582: contig of 1515 bp in length
**	10097: gap of unknown length
**	10196: gap of unknown length
**	10197: contig of 1256 bp in length
**	11453: gap of unknown length
**	11553: gap of unknown length
**	11553: contig of 1096 bp in length
**	12649: gap of unknown length
**	12749: contig of 1385 bp in length
**	14134: gap of unknown length
**	14234: contig of 1318 bp in length
**	15552: gap of unknown length
**	15651: gap of unknown length
**	15652: contig of 1373 bp in length
**	17024: gap of unknown length
**	17124: gap of unknown length
**	17125: contig of 1023 bp in length
**	18148: gap of unknown length
**	18248: contig of 1676 bp in length
**	19924: gap of unknown length
**	20024: contig of 1022 bp in length
**	21046: gap of unknown length
**	21145: contig of 1147 bp in length
**	22293: gap of unknown length
**	22392: contig of 1153 bp in length
**	22393: contig of 1153 bp in length
**	23545: gap of unknown length
**	23546: gap of unknown length
**	23646: gap of unknown length
**	25288: contig of 1643 bp in length
**	25289: gap of unknown length
**	25389: contig of 1600 bp in length
**	26989: gap of unknown length
**	27089: gap of unknown length
**	29136: contig of 2048 bp in length
**	29236: gap of unknown length
**	30361: contig of 1125 bp in length
**	30461: gap of unknown length
**	30462: contig of 1267 bp in length
**	31729: gap of unknown length
**	31828: gap of unknown length
**	33126: contig of 1498 bp in length
**	33327: gap of unknown length
**	33426: gap of unknown length
**	34972: contig of 1546 bp in length
**	35072: gap of unknown length
**	35073: contig of 2026 bp in length
**	37099: gap of unknown length
**	37199: contig of 1678 bp in length
**	38877: gap of unknown length
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**	40521: gap of unknown length
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**	40621: contig of 1092 bp in length
**	41712: gap of unknown length
**	41813: contig of 1899 bp in length
**	43711: contig of 1911 bp in length
**	43812: gap of unknown length
**	45723: gap of unknown length
**	45822: gap of unknown length
**	47647: gap of unknown length
**	47647: gap of 1824 bp in length

Query	Match	Score	DB	Length
Best	Local Similarity	6.1%	45.4%	127354;
Matches	308;	Pred. No.	6.7e-06;	0;
	Conservative	0;	Mismatches	371;
		Indels	0;	Gaps
614	ATCCAGGTAAAGTTAATGTCACACCTTGTCCGGCAATTAAACCTGTAATGTTGCTTAAG	673		
bb	118142 AGCAAGACAACTGAAGGGTTACTACTGCTACTACTGCTACTACTGCTACTACTAG	118201		
674	CTACTTTAGTTAATGTCACATAACCGCATAATGTAACGTGTCATGCCCTGATGGTA	733		
bb	118202 CTGCTTATTACTACTACTACTACTACTACTACTGCTACTACTGCTACTGCTGCTA	118261		
734	CTATAAGTGTGCTGGAGTAATAATTGGTTGACCAAAACACTGAATCTACTATTGTG	793		
bb	118262 CTACTGCTGACTACTACTACTGCTGCTGCTACTACTACTACATGCTGCTACTACTG	118321		
794	CTCCPAACTTTACACATAATAATGTCCTTAATTCAATCCAGGTAATASTACATGCCPAC	853		
bb	118322 CTGCTGCTACTACTACTGCTACTACTGCTACTACTGCTACTACTGCTACTACTG	118381		
854	CTTGGCCAGGAAATAAGGATTATGGTGTGCTGAAGGCACTCAGGNGGTGCGGCTACTTAG	913		
bb	118382 CTACTGCTGCTGCTACTACTACTGCTGCTACTACTGCTACTACTGCTACTACTG	118441		
914	CCAAATAATGAAATAATGCTGCCGATGTTGCAVTTGCAVTTGCAVTTGCAVTTGCA	973		
bb	118442 CTGCTACTACTACTGCTGCTACTACTGCTACTACTGCTACTACTGCTACTACTA	118501		

Qy	974	ATGTAATATTAAACAGAATGCTAAATTGTCGACTTTTGTGAGTAAATA 1033
Db	118502	CATCTGCGCTACTACTACAGCGCTATTACTACTACTGCTACTACTGCTACTA 118561
Qy	1034	ATTCCTAGCCAGGAAGTAGTGTAGATGCCAAACATGCCAGAAATAAAGTTAAAGGCCGTG 1093
Db	118552	CTACTACTGCTACTACTACTGCTACTACTGCTACTACTGCTACTACTGCTACTA 118621
Qy	1094	TAGCAACTGCAAGGTGCTACTGCTACTTAAATTGCTAAATGCGCTCTGCT 1153
Db	118622	CTNGCTACTGCGCTACTACTGCTGCTACTACTGCTGCTACTACTGCTGCTACTA 118681
Qy	1154	GTAATGACTCACCGATGGACAAACATCACTTAAATAAAGCAGCATCTGAAATGCTGTTA 1213
Db	118682	CTACTACTGCTGCTACTACTGCTGCTACTACTGCTGCTACTACTGCTGCTACTA 118741
Qy	1214	AATGTGCGCAACATTAACTACACAAATAAAACTGTTGGTAGCAGTATTGATACT 1273
Db	118742	CTGCTGCTGCTACTACTGCTGCTACTACTGCTGCTACTACTGCTGCTACTACTGCTACTA 118801
Qy	1274	GTAATGTTGAAATAAA 1292
Db	118802	CTACTACTAAATAAA 118820
RESULT 1.3		
AC117361	AC117361	155019 bp DNA clone CH230-228G24, *** linear HTG 18-JUL-2002
LOCUS	Rattus norvegicus	clone CH230-228G24, *** sequencing in progress
DEFINITION	68 unorderd pieces.	
ACCESSION	AC117361	
VERSION	AC117361.4	GI:21746640
KEYWORDS	HTG; HTGS; PHASE1	
SOURCE	Norway rat.	
ORGANISM	Rattus norvegicus	
MATERIALS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus	
1 (bases 1 to 15019)	Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaral, H.C., Are, J.R., Ayele, M., Banks, T., Barbara, J., Benton, J., Bimarge, K., Blaikenburg, K., Bonin, D., Bouch, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coye, M.D., Dathorne, S.R., David, R.R., Davile, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Dein, A.L., Ding, Y., Dinh, B.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, R.J., Earnhardt, C., Edgar, D., Edwards, C.C., Elhaj, C., Escott, M., Falla, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J.J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Guarante, P., Hale, S., Hamilton, K., Harris, C., Harris K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernández, Q., Hodgeson, A., Hogue, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.B., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, U., Korvaj, J., Kovar, C., Krasnicki, J., Kureshi, A., Landry, N., Leah, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichitearage, O., Lieu, C., Liu, J., Liu, W., Louisgeh, H., Lozado, R.J., Lu, X., Lu, Y., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapia, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawlinney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, Z., Mitchell, T., Monhabat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newson, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokonwo, S., Oghu, M., Okwuonu, G., Oraagune, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quilles, M., Ren, Y., Rives, M., Rojas, A., Rotuban, I., Rolfe, M., Ruiz, S., Severy, G., Scherer, S., Scott, G., Shen, H., Shooftari, N., Sisson, H., Sodergran, E., Sonalkar, T., Sparks, A., Staples, H., Stone, H.,	
REFERENCE		
AUTHORS		

Sutton, A., Svatek, A., Tabor, P., Tamerisa, K., Tang, H., Tansy, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usman, K., Vasquez, L., Vera, V., Villano, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczek, R., Woode, S., Worley, K., Wu, C., Wu, Y., Wu, Y.-F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs, R.

Unpublished
2 (bases 1 to 155019)

Worley, K. C.
Direct Submission

Submitted (10-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 155019)

Worley, K. C.
Direct Submission

Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 14, 2002 this sequence version replaced 91:20330656.

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

Project Information
Center project name: GIUB
Center clone name: CH230-228G24

Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 74550 bases at least Q40
Consensus quality: 80029 bases at least Q30
Consensus quality: 84416 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
* NOTE: This is a 'working draft' sequence. It currently
* consists of 68 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1047: contig of 1047 bp in length
* 1147: gap of unknown length
* 1148 2268: contig of 1121 bp in length
* 2269 2368: gap of unknown length
* 2369 3405: contig of 1037 bp in length
* 3406 3505: gap of unknown length
* 3506 4564: contig of 1059 bp in length
* 4565 4664: gap of unknown length
* 4665 5849: contig of 1185 bp in length
* 5850 5949: gap of unknown length
* 5950 7304: contig of 1355 bp in length
* 7305 7404: gap of unknown length
* 7405 8415: contig of 1011 bp in length
* 8416 8515: gap of unknown length
* 8516 9732: contig of 1217 bp in length
* 9733 9832: gap of unknown length
* 9833 10965: contig of 1133 bp in length
* 10966 11065: gap of unknown length
* 11066 12134: contig of 1069 bp in length
* 12135 12234: gap of unknown length
* 12235 13296: contig of 1062 bp in length
* 13297 13396: gap of unknown length
* 13397 14686: contig of 1290 bp in length
* 14687 14786: gap of unknown length

Qy	656	CNGCTAATGTTGCTTGTGCTACTTGTAGTTATGATGCTACATAACCGGATAATGTAACG	715
LOCUS	AC096684	84472 bp	DNA
DEFINITION	Takifugu rubripes clone 241N7, WORKING DRAFT	Linear	HTG 22-SEP-2001
pieces.		SEQUENCE	3 unordered
ACCESSION	AC096684		
VERSION	AC096684_1	GI:115721942	
KEYWORDS	HTGS_PHASE1; HTGS_DRAFT		
SOURCE	Takifugu rubripes		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Takifugu.		
REFERENCE	1 (bases 1 to 84472)		
AUTHORS	Blakesley, R.W., Ayotte, K., Beckstrom-Sternberg, S.M., Benjamin, B., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghjighi, P., Ho, S.-L., Idol, J.R., Karlin, E., Laric, P., Lee-Lin, S.-Q., Legaspí, R., Maduro, Q.L., Maduro, V.B., Masiello, C., Mastran, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Zhang, L.-H. and Green, E.D.		
TITLE	NISC Comparative Sequencing Initiative		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 84472)		
AUTHORS	Green, E.D.		
JOURNAL	Direct Submission		
COMMENT	Submitted (22-SEP-2001) NIH Intramural Sequencing Center, 8717 Grovermont Circle, Gaithersburg, MD 20877, USA		
REFERENCE	3 (bases 1 to 84472)		
AUTHORS	Green, E.D.		
JOURNAL	NIH Intramural Sequencing Center		
COMMENT	Center: NIH Intramural Sequencing Center Center code: NISC Web site: http://www.nisc.nih.gov Contact: nisc.mouseinigrn.nih.gov Project Information Center project name: arc Center clone name: 241N07 Summary Statistics Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 83639 bases at least Q30 Consensus quality: 83900 bases at least Q30 Insert size: 89000; agarose-fp Insert size: 84272; sum-of-contigs Quality coverage: 12.81x in Q20 bases; agarose-fp Quality coverage: 11.23x in Q20 bases; pulse-field-gel Quality coverage: 13.53x in Q20 bases; sum-of-contigs		
NOTE	This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.		
1	10947: contig of 10947 bp in length		
10948	11047: gap of unknown length		
10949	37666: contig f_66510		

